

30.APR.2002 18:07

O BIOCHEMISTRY 643 479 7866

wednesday, 30 April 2002

O U BIOCHEMISTRY



results of BLAST

TBLASTN 2.2.3 [Apr-24-2002]

References:
 Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
 Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
 "Gapped BLAST and PSI-BLAST: a new generation of protein database search
 programs", Nucleic Acids Res. 25:3389-3402.

RID: 1020140625-011436-28352

Query=
 (324 letters)

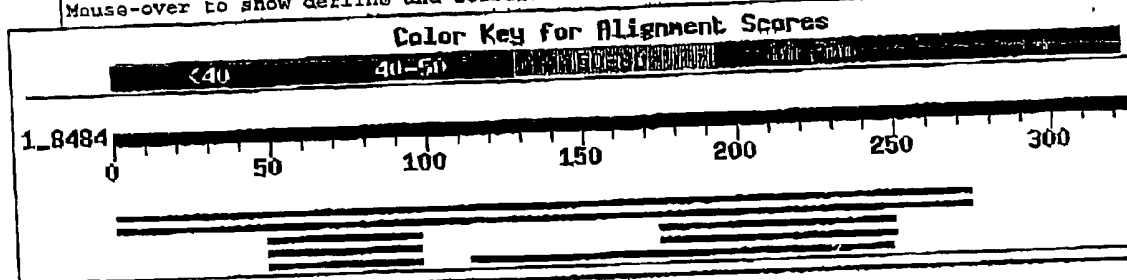
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
 GSS, or phase 0, 1 or 2 HTGS sequences)
 1,218,445 sequences; 5,427,962,278 total letters

If you have any problems or questions with the results of this search
 please refer to the **BLAST FAQ**

Taxonomy reports

Distribution of 9 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
 (bits) Value

gi 2636718 gb AF007776.1 AF007776	Candida albicans	549	e-154
gi 3273716 gb AF050216.1 AF050216	Candida albicans chromoso...	549	e-154
gi 13366236 gb U22831.2	Caenorhabditis elegans cosmid F47D...	40	0.30
gi 17553483 ref NM_065980.1	Caenorhabditis elegans	40	0.30
gi 20197171 gb AC005397.3	Arabidopsis thaliana chromosome ...	32	4.1
gi 1754514 gb D87515.1 D87515	Rattus norvegicus mRNA for a...	35	9.7
gi 13592046 ref NM_031097.1	Rattus norvegicus aminopeptida...	35	9.7
gi 2039142 gb U61696.1 RN061696	Rattus norvegicus aminopept...	35	9.7

Alignments

>gi|2636718|gb|AF007776.1|AF007776 Candida albicans
 Length = 6426

Score = 549 bits (1415), Expect = e-154
 Identities = 272/274 (99%). Positives = 272/274 (99%)
 Frame = +2

Query: 1 MSSAKNDDEGKVMESVDQANAI SKVDEHIKARFNMLFIKFNDL PKLAVGNQKSVQKWE 60
 MSSAKNDDEGKVMESVDQANAI SKVDEHIKARFNMLFIKFNDL PKLAVGNQKSVQKWE
 Sbjct: 398 MSSAKNDDEGKVMESVDQANAI SKVDEHIKARFNMLFIKFNDL PKLAVGNQKSVQKWE 577

Query: 61 EFKYPHVAYPDVLEFLLDYNNPKDKFKVKKVVEGIYPTGWCLQMCLOSIQFDRFRLLIMISKLE 120
 EFKYPHVAYPDVLEFLLDYNNPKDKFKVKKVVEGIYPTGWCLQMCLOSIQFDRFRLLIMISKLE
 Sbjct: 578 EFKYPHVAYPDVLEFLLDYNNPKDKFKVKKVVEGIYPTGWCLQMCLOSIQFDRFRLLIMISKLE 757

Query: 121 KHLQKEANLIKAAYDAVTKSKDYTTITSKILSKFVNVEHELVCYNLPYLSQVEEKLEIL 180
 KHLQKEANLIKAAYDAVTKSKDYTTITSKILSKFVNVEHELVCYNLPYLSQVEEKLEIL
 Sbjct: 758 KHLQKEANLIKAAYDAVTKSKDYTTITSKILSKFVNVEHELVCYNLPYLSQVEEKLEIL 937

Query: 181 YNTSNVVDYVRSPLNLIQGVLYFNHVKKSEALSLFLNIHASYYSKWIQADNDTSVLPSC 240
 YNTSNVVDYVRSPLNLIQGVLYFNHVKKSEALSLFLNIHASYYSKWIQADNDTSVLPSC

Received Time 30.Apr. 18:38
<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

30 APR 2002 18:07

O U BIOCHEMISTRY 643 479 7866

uesday, 30 April 2002

O U BIOCHEMISTRY RYSKWIQADNDTSVLPSC 1117

Query: 938 YNTSNVDEYVRSLFNLIGQVLY
Query: 241 STIAEMCDHPDYARLVDIPSNNKYELNLIVSLPA 274
STIAEMCDHPDYARLVDIPSNNKYELNLIVSLPA
Sbjct: 1118 STIAEMCDHPDYARLVDIPSNNKYELNLIVSLPA 1219

>gi|1273716|gb|AF050215.1|AF050215 Candida albicans chromosome 3 map between CDR1 and DYN1 strain
HOG759
Length = 6980

Score = 549 bits (1415), Expect = e-154
Identities = 272/274 (99%), Positives = 272/274 (99%)
Frame = +1

Query: 1 MSSAKNDDNEGKVMESVDQANAI SKVDEHIKARFNMLFIKFNLDLPKLAVGNQKSVDKWNE 60
MSSAKNDDNEGKVMESVDQANAI SKVDEHIKARFNMLFIKFNLDLPKLAVGNQKSVDKWNE
Sbjct: 604 MSSAKNDDNEGKVMESVDQANAI SKVDEHIKARFNMLFIKFNLDLPKLAVGNQKSVDKWNE 783

Query: 61 EFKYFHVAYPDVLEFLLDYNEKDKFKVKKVEGIYFTGWCLQMCLOSIFDRFRLIMISKLP 120
EFKYFHVAYPDVLEFLLDYNEKDKFKVKKVEGIYFTGWCLQMCLOSIFDRFRLIMISKLP
Sbjct: 784 EFKYFHVAYPDVLEFLLDYNEKDKFKVKKVEGIYFTGWCLQMCLOSIFDRFRLIMISKLP 963

Query: 121 KHLQKEANLIKAAYDAVTKSKDYTTITSKILSKFVNVEHELVCYNLPYLQVEKLEBIL 180
KHLQKEANLIKAAYDAVTKSKDYTTITSKIL KPVNVEHELVCYNLPYLQVEKLEBIL
Sbjct: 964 KHLQKEANLIKAAYDAVTKSKDYTTITSKIL KPVNVEHELVCYNLPYLQVEKLEBIL 1143

Query: 181 YNTSNVDEYVRSLFNLIGQVLYFNVHVKSEALSLFLNIHASYYSKWIQADNDTSVLPSC 240
YNTSNVDEYVRSLFNLIGQVLYFNVHVKSEALSLFLNIHASYYSKWIQADNDTSVLPSC
Sbjct: 1144 YNTSNVDEYVRSLFNLIGQVLYFNVHVKSEALSLFLNIHASYYSKWIQADNDTSVLPSC 1323

Query: 241 STIAEMCDHPDYARLVDIPSNNKYELNLIVSLPA 274
STIAEMCDHPDYARLVDIPSNNKYELNLIVSLPA
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>gi|13356236|gb|U22631.2| Caenorhabditis elegans cosmid F47D12, complete sequence
Length = 42275

Score = 40.0 bits (92), Expect = 0.30
Identities = 24/80 (30%), Positives = 36/80 (45%), Gaps = 4/80 (5%)
Frame = -1

Query: 175 KLEBILYNTSNVDEYVRSLF----NLIGQVLYFNVHVKSEALSLFLNIHASYYSKWQA 230
K I N + +D S+P NL + YFNH+ K + + IH S+Y WI
Sbjct: 18740 KKNISINIDSKLDMTWCISIPLNSSNLYCCIRYFNHPIKIRSTGCW--IHKSPYLNWIHF 18567

Query: 231 DNDTSVLPSCSTIAEMCDH 250
+ V P T+ ++ DH
Sbjct: 18566 STNKKVKPCVLTVERQLVDH 18507

>gi|17553483|ref|NM_065980.1| L Caenorhabditis elegans
Length = 423

Score = 40.0 bits (92), Expect = 0.30
Identities = 24/80 (30%), Positives = 36/80 (45%), Gaps = 4/80 (5%)
Frame = -1

Query: 175 KLEBILYNTSNVDEYVRSLF----NLIGQVLYFNVHVKSEALSLFLNIHASYYSKWQA 230
K I N + +D S+P NL + YFNH+ K + + IH S+Y WI
Sbjct: 224 KKNISINIDSKLDMTWCISIPLNSSNLYCCIRYFNHPIKIRSTGCW--IHKSPYLNWIHF 61

Query: 231 DNDTSVLPSCSTIAEMCDH 250
+ V P T+ ++ DH
Sbjct: 60 STNKKVKPCVLTVERQLVDH 1

>gi|20197371|gb|AC006387.3| Arabidopsis thaliana chromosome 2 clone T3F17 map CIC02E07, complete
sequence
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Frame = +3

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I++ L K L K ++ Y + +S+ T T++S +V++ ++ + +S ++
Sbjct: 48288 ILMQLLVKGL-KLTMVATYI-RYQSRISITTEVTSTWVLLR*VLCKSPISISYLK 48464

Query: 174 EKLEBILYNTSNVDEYVRSLFNLIGQVLYFNVHVKSEALSLFLNIHASYYSK----WQ 229
E ++ + + N+ + + + +V Y N++ A + LN+ S YS+ W+Q
Sbjct: 48465 EVIQLV--SGNIDQKRMGCISECRKRVSYQNNIS*BEAFDVLLNVLMSIYGRIPGHVWQ 48635

Score = 22.7 bits (47), Expect(2) = 4.1
Identities = 7/17 (41%), Positives = 12/17 (70%)
Frame = +1

Query: 233 DTSVLPSCSTIAEMCD 249
D+ +L SC+T+ +CD
Sbjct: 48715 DSRILVSCNTLYSRLCD 48765

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30.APR.2002 18:08

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RID=1020140023-011400-20002.

uesday, 30 April 2002

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Rattus norvegicus mRNA for aminopeptidase-B, complete cds

>gi|1754514|gb|U07515.1|U07515
Length = 2192Score = 35.0 bits (79), Expect = 9.7
Identities = 21/55 (38%), Positives = 30/55 (54%), Gaps = 5/55 (9%)
Frame = +3Query: 49 VGNQKSVDK---WNEEFKYFHVAYPDVLEFLDYNNPKDKFK-VKKVGGIYFTGW 98
VG+Q+ DK + +EFK+ + D LEP L+Y P+ K K V + G F W
Sbjct: 1284 VGDQEQFDKFLKAYVDEPKFQSILAEDEFLEFYLEYFPELKKKGVDSTPGFEFNRW 1448>gi|13592046|ref|NM_031097.1|U Rattus norvegicus aminopeptidase B (Rnpep), mRNA
Length = 2208Score = 35.0 bits (79), Expect = 9.7
Identities = 21/55 (38%), Positives = 30/55 (54%), Gaps = 5/55 (9%)
Frame = +3Query: 49 VGNQKSVDK---WNEEFKYFHVAYPDVLEFLDYNNPKDKFK-VKKVGGIYFTGW 98
VG+Q+ DK + +EFK+ + D LEP L+Y P+ K K V + G F W
Sbjct: 1287 VGDQEQFDKFLKAYVDEPKFQSILAEDEFLEFYLEYFPELKKKGVDSTPGFEFNRW 1451>gi|2039142|gb|U61696.1|U61696 Rattus norvegicus aminopeptidase B mRNA, complete cds
Length = 2208Score = 35.0 bits (79), Expect = 9.7
Identities = 21/55 (38%), Positives = 30/55 (54%), Gaps = 5/55 (9%)
Frame = +3Query: 49 VGNQKSVDK---WNEEFKYFHVAYPDVLEFLDYNNPKDKFK-VKKVGGIYFTGW 98
VG+Q+ DK + +EFK+ + D LEP L+Y P+ K K V + G F W
Sbjct: 1287 VGDQEQFDKFLKAYVDEPKFQSILAEDEFLEFYLEYFPELKKKGVDSTPGFEFNRW 1451Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,
or phase 0, 1 or 2 HTGS sequences)
Posted date: Apr 29, 2002 1:59 AM
Number of letters in database: 1,132,994,982
Number of sequences in database: 1,218,445Lambda K H
0.317 0.134 0.368Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1,648,687,762

Number of Sequences: 1218445

Number of extensions: 24413213

Number of successful extensions: 103318

Number of sequences better than 10.0: 16

Number of HSP's better than 10.0 without gapping: 38293

Number of HSP's successfully gapped in prelim test: 5836

Number of HSP's that attempted gapping in prelim test: 52250

Number of HSP's gapped (non-prelim): 69771

length of query: 324

length of database: 1,809,320,759

effective HSP length: 136

effective length of query: 188

effective length of database: 1,643,612,239

effective search space: 308999100932

effective search space used: 308999100932

frameshift window, decay const: 50, 0.1

T: 13

A: 40

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 79 (35.0 bits)

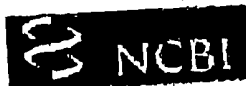
30. APR. 2002 18:05

O U BIOCHEMISTRY 643 479 7866

Wednesday, 30 April 2002

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Nucleotide



Search Nucleotide for

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Related Sequences, Protein, Taxonomy

1: AF050215. Candida albicans ...[gi:3273716]

LOCUS AF050215 6980 bp DNA linear PLN 01-JUL-1998
DEFINITION Candida albicans Tsa2 retrotransposon gag polyprotein (gag) and pol polyprotein (pol) genes, complete cds.
ACCESSION AF050215
VERSION AF050215.1 GI:3273716
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SOURCE Candida albicans.
ORGANISM Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE 1 (bases 1 to 6980)
AUTHORS Goodwin, T.J.D. and Poulter, R.T.M.
TITLE Temperature- and strain-dependent expression of the pCal
retrotransposon of Candida albicans
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 6980)
AUTHORS Goodwin, T.J.D. and Poulter, R.T.M.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-1998) Department of Biochemistry, University of
Otago, Cumberland Street, Dunedin, New Zealand
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/protein_id="AAC24821.1"
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PSEESLECDPDDVGLADMLSNAGDDDKKSKSNEMSEYQEHYSSRALINSLTEVDL
DVRISPYGVEQLLPTGDNDIYNPHLMSNMHSTKILLCKYGGVLTSTKESLQKIA
DCKVCLLSNAKQRSHMPHSEKASRHERLHCDTIGFPRSENKWLTSVIDEHTGYT
EGYITKQKVKDILLQELKIVNNRPNKQVAYFRSDNABRFPQPSDLAEFGIWRETIA
YSTELNGLAEVNNKILQOTYKIVVTLGPPQILKLYTYVQYSITNINHTPRRSLKGT
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mbez/query.fag?cmd=RefView&db=nucleotide&file_id=3273718&dept=Campark

Wednesday, 30 April 2002

misc feature

2447 B

[illegible]

Received Time 30 Apr. 18:38

[http://www.fishbase.org/cgi-bin/species.cgi?id=227371&api=](#)

O U BIOCHEMISTRY 643 479 7866

30. APR. 2002 18:06

Monday, 30 April 2002

4261 atcccttgcgc ataaagagact ggaacg U BIOCHEMISTRY: gacga aattggagact
4321 ggcatttaatt agcagcagcat tgcctgaaggt aacccactac cagatggaad taagtgatgct
4381 cagatgaatc agagcttttga taatcaatcac agcatgtcac gaggcaagaa gaatatagaca
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Revised: October 24, 2001.

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